

ABSTRACT

That invention provides a nucleic acid information detection method which, in a method wherein a target nucleic acid, and probes having a complementary sequence with at least a portion of the target nucleic acid sequence, are contacted with each other in order to form hybrids between the target nucleic acid and the probes, and the amount of signal generated depending on the amount of hybrids is measured in order to detect the information on the target nucleic acid, includes kinetically obtaining data of the signal.

Furthermore the invention provides a nucleic acid information detection method which, in a method wherein a perfect matched probe having a perfect complementary sequence with respect to at least part of a target nucleic acid sequence, and one or more types of imperfectly matched probes having at least one part of the perfect matched probe mutated, are contacted with the target nucleic acid in order to hybridize between the target nucleic acid and the perfect matched probe, or the imperfect matched probes, so that the information on the target nucleic acid can be detected based on the difference in binding strength of the hybrids, includes kinetically obtaining data of the signal while changing continuously or stepwise the condition for measuring or detecting the signal from the hybrids.